



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 135120

TO: Nita M Minnifield
Location: REM-3C01-3C18
Art Unit: 1645
Tuesday, October 19, 2004

Case Serial Number: 10/034623

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

*Reviewed
12/15/04*

135/20

STIC-Biotech/ChemLib

From: Minnifield, Nita
Sent: Friday, October 15, 2004 8:41 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

10/034623

STIC

Please do a commercial and interference sequence search on SEQ ID NO: 6 of the above application.

Please provide a paper copy of the results.

Thanks,
Minnifield
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 10/18/04
Date Completed: 10/19/04
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # 1
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: Q2P
WWW/Internet: _____
Other(Specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2004, 14:31:31 ; Search time 189 Seconds

(without alignments)
818,919 Million cell updates/sec

Title: US-10-034-623-6

Sequence: 1 MHGIEGRGDMSENFVAFV.....RPAKKTGRRARRAARRR 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: Uniprot 02:*

2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1357	100.0	269	2 074057	074057 cenarchaeum
2	220.5	16.2	221	1 HC2X_CHLTR	Q46397 chlamydia t
3	219	16.1	207	1 HCT2_CHLTR	P38020 chlamydia m
4	215	15.8	225	2 07WFA2	07WFA2 bordetella
5	208	15.3	376	2 082KM1	082KM1 streptomyce
6	204	15.0	201	1 HC2D_CHLTR	066280 chlamydia t
7	203.5	15.0	172	1 HCT2_CHLTR	Q22819 chlamydia p
8	201.5	14.8	197	2 07W3X2	07W3X2 bordetella
9	201	14.8	328	1 SSS3_DROER	P13730 diosiphella
10	200.5	14.8	175	2 07VUT9	Q74570 bordetella
11	199.5	14.7	182	2 045370	Q45370 bordetella
12	198	14.6	177	2 06SG84	06SG84 uncultured
13	198	14.6	177	2 AAR37978	AAR37978 uncultured
14	196.5	14.5	454	2 06IT77	06IT77 spissula sol
15	194.5	14.3	155	2 08P140	08P140 xanthomonas
16	193	14.2	156	2 08P6U0	08P6U0 xanthomonas
17	192	14.1	455	2 06IT76	06IT76 spissula sol
18	190.5	14.0	200	2 08XVW7	08XVW7 chlamydia s
19	187.5	13.8	152	2 0823J8	0823J8 chlamydia s
20	186	13.7	152	2 09XYV7	09XYV7 euplotes cr
21	177	13.0	217	2 08ZUS0	08ZUS0 streptomyce
22	176.5	13.0	283	2 08PFR2	08PFR2 xanthomonas
23	174.5	12.9	273	2 07VAY8	07VAY8 prochloroc
24	174	12.8	165	1 HC2B_CHLTR	066281 chlamydia t
25	172	12.7	422	2 086GB1	086GB1 anopheles s
26	172	12.7	753	2 06PEP4	06PEP4 brachydanio
27	169	12.5	218	1 AAR57473	AAR57473 brachydan
28	169	12.5	966	2 0747I8	0747I8 streptomyce
29	169	12.5	966	2 AAR36668	AAR36668 geobacter s
30	163.5	12.0	505	2 Q24898	Q24898 ensis minor

32	163	12.0	371	2 06N4V4	Q6N4V4 rhodopseudo
33	163	12.0	371	2 CAE28670	CAE28670 rhodopseu
34	160.5	11.8	356	2 08ZAC8	08ZAC8 streptomyce
35	160.5	11.8	435	2 07RTL5	07RTL5 anopheles g
36	159.5	11.8	329	2 08BRD8	08BRD8 pseudomonas
37	158	11.6	237	2 091S26	091S26 regina rana
38	158	11.6	275	2 06YH51	06YH51 ambystoma t
39	158	11.6	275	2 AAR33252	AAR33252 ambystoma
40	156.5	11.5	259	2 08P419	08P419 xanthomonas
41	156	11.5	182	2 08RL36	08RL36 burkholderi
42	156	11.5	379	2 07WFN5	07WFN5 bordetella
43	155.5	11.5	212	2 073V19	073V19 mycobacteri
44	155.5	11.5	212	2 AAR0572	AAR0572 mycobacte
45	155	11.4	209	2 08PBM2	08PBM2 xanthomonas

ALIGNMENTS

RESULT 1	ID	074057	PRELIMINARY;	PRT;	269 AA.
AC	074057				
DT	01-NOV-1998	(TREMBLrel. 08, Created)			
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)			
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)			
DE	Histone H1 DNA binding protein.				
GN	Name=hc2;				
OS	Cenarchaeum symbiosum.				
OC	Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeaceae;				
OC	Cenarchaeum.				
OX	NCBI_TaxID=46770;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=B;				
RX	MEDLINE=98422450; PubMed=9748430;				
RA	Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,				
RA	Swanson R.V.;				
RT	"Genomic analysis reveals chromosomal variation in natural populations				
RT	of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";				
RL	J. Bacteriol. 180:5003-5009(1998).				
DR	EMBL; AF083072; AAC62700.1;				
DR	PIR; T31309; T31309.				
SO	SEQUENCE 269 AA; 29889 MW; ADCADCT50DACGB8 CRC64;				

Query Match 100.0%; Score 1357; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.1e-91;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MHGIEGRGDMSENFVAFVACARGVTKDMMKYDGRVHHKECHARRHGQIREPNEVEQ	60
DB	1	MHGIEGRGDMSENFVAFVACARGVTKDMMKYDGRVHHKECHARRHGQIREPNEVEQ	60
QY	61	RVAELEKVDLIQMNQLAEMNRASGDGVSATSAEAEOHAELEKVOVMNQLAEMN	120
DB	61	RVAELEKVDLIQMNQLAEMNRASGDGVSATSAEAEOHAELEKVOVMNQLAEMN	120
QY	121	RAPGKPAKKAAGTARRKSGKTVRRKRTAGKKAAGARRKTTAKKA	180
DB	121	RAPGKPAKKAAGTARRKSGKTVRRKRTAGKKAAGARRKTTAKKA	180
QY	181	AKRGKAPKATVTKTVHKKIGVRRKTTARRTAGSTVRKSTVTKTVHRRKTKAVRR	240
DB	181	AKRGKAPKATVTKTVHKKIGVRRKTTARRTAGSTVRKSTVTKTVHRRKTKAVRR	240
QY	241	KSTVKTARRPAGKRTGPAARRAARRR	269
DB	241	KSTVKTARRPAGKRTGPAARRAARRR	269

RESULT 2
HC2X_CHLTR
ID HC2X_CHLTR STANDARD; PRT; 221 AA.

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OM protein - protein search, using sw model

Run on: October 18, 2004, 14:39:24 ; Search time 40 Seconds

(without alignments)
647,058 Million cell updates/sec

Title: US-10-034-623-6

Sequence: 1 MGIIEGGRGDMSENFAVCV.....RPAKRTTPGAAARRAKARR 269

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1357	100.0	269	2	histone H1 DNA bin
2	220.5	16.2	223	2	histone H1 homolog
3	219	16.1	207	2	Hc2 nucleoprotein
4	217	16.0	207	2	histone H1 homolog
5	204	15.0	203	2	probable histone-1
6	203.5	15.0	172	2	histone-like prote
7	203.5	15.0	172	2	histone-like prote
8	201	14.8	328	2	histone H1 homolog
9	199.5	14.7	182	2	histone H1 homolog
10	174	12.8	165	2	histone H1 homolog
11	169	12.5	218	2	histone H1 homolog
12	154	11.3	1390	2	histone H1-like DNA b
13	153	11.3	248	1	histone H1, gonada
14	152.5	11.2	288	2	histone H1, gonada
15	151.5	11.2	1052	1	histone H1, gonada
16	151.5	11.2	1701	2	histone H1, gonada
17	148	10.9	135	2	histone H1, gonada
18	148	10.9	229	2	histone H1, gonada
19	145.5	10.7	221	2	histone H1, gonada
20	142.5	10.5	282	2	histone H1, gonada
21	142.5	10.5	284	2	histone H1, gonada
22	140.5	10.4	241	2	histone H1, gonada
23	139	10.2	1403	2	histone H1, gonada
24	138.5	10.2	384	2	histone H1, gonada
25	138.5	10.2	1773	2	histone H1, gonada
26	138.5	10.2	1815	2	histone H1, gonada
27	136.5	10.1	421	2	histone H1, gonada
28	136	10.0	256	2	histone H1, gonada
29	136	10.0	289	2	histone H1, gonada

30	136	10.0	365	2	T35620
31	136	10.0	1203	2	S26650
32	134	9.9	309	2	G83013
33	132.5	9.8	214	2	G70673
34	132	9.7	206	2	S09388
35	132	9.7	952	2	T36664
36	131	9.7	485	2	T13479
37	130.5	9.6	239	2	T34945
38	129	9.5	239	2	T34733
39	129	9.5	289	2	A81779
40	127	9.4	352	2	G82990
41	127	9.4	510	1	S41307
42	127	9.4	528	2	B75310
43	126.5	9.3	271	2	T06392
44	126.5	9.3	1173	2	T31421
45	126	9.3	210	2	A25550

ALIGNMENTS

RESULT 1

T31309

histone H1 DNA binding protein - Cenarchaeum symbiosum

C/Species: Cenarchaeum symbiosum

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C/Accession: T31309

R/Schleper, C.; Delong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.

J. Bacteriol. 180, 5003-5009, 1998

A/Title: Genomic analysis reveals chromosomal variation in natural populations of the

A/Reference number: Z20994, M01D:98422450, PMID:9748430

A/Accession: T31309

A/Status: Preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-269 <SCH>

A/References: UNIPROT:074057; EMBL:AF083072; NID:g3599393; PID:g3599395; PIDN:AF

A/Genes: hc2

Query Match 100.0%; Score 1357; DB 2; Length 269;

Best Local Similarity 100.0%; Pred No. 1.7e-86;

Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGIIEGGRGDMSENFAVCVACARGVTKDQEMKYVDGRVFRHKECHARRGGQIRFNPVEVQ	60
DB	1	MGIIEGGRGDMSENFAVCVACARGVTKDQEMKYVDGRVFRHKECHARRGGQIRFNPVEVQ	60
QY	61	RVAEELKVDLIQWENQIAEMNRASGDGCHSSATSAAEAEOHRAELVQIOWMNQIAEMN	120
DB	61	RVAEELKVDLIQWENQIAEMNRASGDGCHSSATSAAEAEOHRAELVQIOWMNQIAEMN	120
QY	121	RAAPGKPAKKAAGTARRKSGKTVRRRTGRTGKAGARRKTVARRKTTAKKA	180
DB	121	RAAPGKPAKKAAGTARRKSGKTVRRRTGRTGKAGARRKTVARRKTTAKKA	180
QY	181	AGKAGARRKATVKTTHKIGVRRKTTARRTAGSTVRRKSTVTKTVARRKTKKAVVR	240
DB	181	AGKAGARRKATVKTTHKIGVRRKTTARRTAGSTVRRKSTVTKTVARRKTKKAVVR	240
QY	241	KSTVRRTPARRPAGKRTTPGAAARRAKARR	269
DB	241	KSTVRRTPARRPAGKRTTPGAAARRAKARR	269

RESULT 2

A36884

histone H1 homolog Hc2 - Chlamydia trachomatis

C/Species: Chlamydia trachomatis

C/Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004

C/Accession: A36884, JN0851

A/Title: Molecular cloning and expression of hctB encoding a strain-variant chlamydial

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OM protein - protein search, using SW model

Run on: October 18, 2004, 14:28:24 ; Search time 132 Seconds
(without alignments)
658.885 Million cell updates/sec

Title: US-10-034-623-6

Perfect score: 1357

Sequence: 1 MHGIEGGRGDMSENFVAFV.....RPAGKTPGARAPRAGAKRR 269

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1357	100.0	269	US-10-027-806-6	Sequence 6, Appl1
2	1357	100.0	269	US-10-034-623-6	Sequence 6, Appl1
3	1357	100.0	269	US-10-027-801-6	Sequence 6, Appl1
4	1357	100.0	269	US-10-029-120-6	Sequence 6, Appl1
5	208	15.3	376	US-10-156-761-9889	Sequence 9889, Ap
6	204	15.0	203	US-09-820-843A-7	Sequence 7, Appl1
7	203.5	15.0	172	US-09-820-843A-5	Sequence 5, Appl1
8	203.5	15.0	182	US-10-289-762-402	Sequence 402, App
9	177	13.0	217	US-10-156-761-10221	Sequence 10221, A
10	160.5	11.8	356	US-10-156-761-13658	Sequence 13658, A
11	159.5	11.8	329	US-10-282-122A-67699	Sequence 67699, A
12	155.5	11.5	212	US-10-282-122A-61735	Sequence 61735, A
13	154	11.3	969	US-10-282-122A-50758	Sequence 50758, A
14	152.5	11.2	301	US-10-437-963-182491	Sequence 182491, A

15	149.5	11.0	289	US-10-437-963-144785	Sequence 144785, App
16	148	10.9	223	US-10-051-643-201	Sequence 201, App
17	148	10.9	223	US-10-205-979-52	Sequence 52, Appl1
18	148	10.9	1387	US-10-156-761-13000	Sequence 13000, A
19	147.5	10.9	260	US-10-437-963-107671	Sequence 107671, A
20	146.5	10.8	366	US-10-156-761-10482	Sequence 10482, A
21	145.5	10.7	184	US-10-424-599-188977	Sequence 188977, A
22	140	10.3	337	US-10-437-963-157680	Sequence 157680, A
23	139	10.2	19608	US-10-084-846A-8	Sequence 8, Appl1
24	138.5	10.2	428	US-10-282-122A-55748	Sequence 55748, A
25	138.5	10.2	446	US-10-437-963-127362	Sequence 127362, A
26	138.5	10.2	1773	US-10-282-122A-65817	Sequence 65817, A
27	138	10.2	279	US-10-181-071-7	Sequence 7, Appl1
28	137.5	10.1	942	US-10-156-761-12155	Sequence 12155, A
29	137	10.1	2263	US-10-408-765A-2231	Sequence 2231, Ap
30	136.5	10.1	421	US-10-282-122A-56483	Sequence 56483, A
31	136	10.0	211	US-10-437-963-174659	Sequence 174659, A
32	136	10.0	228	US-10-156-761-9425	Sequence 9425, Ap
33	136	10.0	321	US-09-864-761-33718	Sequence 33718, A
34	136	10.0	361	US-09-864-761-33614	Sequence 33614, A
35	136	10.0	361	US-09-864-761-33614	Sequence 33614, A
36	136	10.0	1047	US-10-029-386-33522	Sequence 33522, A
37	136	10.0	1087	US-10-029-386-32407	Sequence 32407, A
38	135.5	10.0	202	US-10-437-963-151115	Sequence 151115, A
39	135.5	10.0	204	US-10-437-963-151115	Sequence 151115, A
40	135.5	10.0	838	US-10-156-761-10342	Sequence 10342, A
41	135	9.9	221	US-10-424-599-252204	Sequence 252204, A
42	134.5	9.9	315	US-10-437-963-200938	Sequence 200938, A
43	134.5	9.9	503	US-10-282-122A-50517	Sequence 50517, A
44	134	9.9	251	US-10-437-963-180341	Sequence 180341, A
45	134	9.9	309	US-09-820-843A-24	Sequence 24, Appl1

ALIGNMENTS

RESULT 1	US-10-027-806-6	US-10-027-806-6
Publication No.	US20020160476A1	US10027806
GENERAL INFORMATION:		
APPLICANT:	Swanson, Ronald V.	
APPLICANT:	Feldman, Robert A.	
APPLICANT:	Schleper, Christa	
TITLE OF INVENTION:	NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM	
FILE REFERENCE:	DCORP.002A	
CURRENT APPLICATION NUMBER:	US/10/027,806	
CURRENT FILING DATE:	2001-12-21	
PRIOR APPLICATION NUMBER:	EARLIER APPLICATION NUMBER: 09/408,020	
PRIOR FILING DATE:	EARLIER FILING DATE: 1999-09-23	
NUMBER OF SEQ ID NOS:	123	
SOFTWARE:	FastSeq for Windows Version 3.0	
SEQ ID NO 6		
LENGTH:	269	
TYPE:	PRT	
ORGANISM:	Cenarchaeum symbiosum	
US-10-027-806-6		
Query Match	100.0%; Score 1357; DB 13; Length 269;	
Best Local Similarity	100.0%; Pred. No. 3.5e-113;	
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MHGIEGGRGDMSENFVAFVCAACRGRTYDEMKTVDGRVFFKECHARRGGQIRPNPEVEQ 60	
DB	1 MHGIEGGRGDMSENFVAFVCAACRGRTYDEMKTVDGRVFFKECHARRGGQIRPNPEVEQ 60	
QY	61 RVAELVYDILQMNQLAENNRASGDGVHSATSAAAEQHRALVKVQLQVMNQLAENM 120	
DB	61 RVAELVYDILQMNQLAENNRASGDGVHSATSAAAEQHRALVKVQLQVMNQLAENM 120	
QY	121 RPAKGPAPKAAAGKATARRSKGKTVRRKTKRTAGKKAAGARRKTVKRTARRKTTAKKA 180	
DB	121 RPAKGPAPKAAAGKATARRSKGKTVRRKTKRTAGKKAAGARRKTVKRTARRKTTAKKA 180	

WZCF06TC/CO WOTMCTDF; IZC

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 19, 2004, 14:30:38 ; Search time 160 Seconds
(without alignments)
603.114 Million cell updates/sec

Title: US-10-034-623-6

Perfect score: 1357

Sequence: 1 MHGIEGGRGDMSENFVAFCV.....PPAGKTPGRARARAGAKRR 269

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: Geneseqp1980s:*
2: Geneseqp1980s:*
3: Geneseqp2000s:*
4: Geneseqp2000s:*
5: Geneseqp2000s:*
6: Geneseqp2000s:*
7: Geneseqp2000s:*
8: Geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1357	100.0	269	3	AAV90914
2	226	16.7	295	2	AAV37179
3	204	15.0	203	7	ABO23506
4	203.5	15.0	172	7	ABO23504
5	203.5	15.0	182	2	AAV34984
6	159.5	11.8	329	6	ABU33775
7	155.5	11.3	212	6	ABU33811
8	154	11.3	969	6	ABU22834
9	153	11.2	290	2	AAV38693
10	151.5	11.2	540	4	ADM19717
11	148	10.9	223	2	AAV14928
12	148	10.9	223	6	ABP70903
13	147	10.8	246	7	ABO67840
14	146	10.8	252	3	AAV74897
15	145.5	10.7	583	3	ABG09005
16	144.5	10.6	267	2	AAV38692
17	144.5	10.6	267	2	AAV38692
18	141	10.4	1275	4	ABG20340
19	140	10.3	289	4	ABP80636
20	139	10.2	467	5	ABP69558
21	139	10.2	1098	6	ABG20365
22	138.5	10.2	428	6	ABU27824
23	138.5	10.2	1773	6	ABU37893
24	138	10.2	279	4	AAU03592
25	138	10.2	467	4	ABP94309

26	137.5	10.1	392	2	AAV96808	AAV96808 Neisseria
27	137.5	10.1	492	7	ABO79593	ABO79593 Pseudomon
28	137	10.1	266	7	AAV74898	AAV74898 Neisseria
29	137	10.1	956	6	ABO53053	ABO53053 Human put
30	137	10.1	2263	7	ADJ70425	ADJ70425 Human hea
31	136.5	10.1	421	6	ABU28559	ABU28559 Protein e
32	136	10.0	289	2	AAV38690	AAV38690 Neisseria
33	136	10.0	321	4	AAV14001	AAV14001 Peptide #
34	136	10.0	321	4	ABP32946	ABP32946 Peptide #
35	136	10.0	321	4	AAV26407	AAV26407 Peptide #
36	136	10.0	321	4	ABP27775	ABP27775 Human pep
37	136	10.0	321	4	ABP18420	ABP18420 Protein #
38	136	10.0	321	4	AAV6130	AAV6130 Human bon
39	136	10.0	321	4	AAV5747	AAV5747 Human bra
40	136	10.0	321	4	ABG47798	ABG47798 Human liv
41	136	10.0	321	4	AAV01742	AAV01742 Peptide #
42	136	10.0	321	5	ABG35780	ABG35780 Human pep
43	136	10.0	361	4	AAV14436	AAV14436 Peptide #
44	136	10.0	361	4	AAV13889	AAV13889 Peptide #
45	136	10.0	361	4	ABP32834	ABP32834 Peptide #

ALIGNMENTS

RESULT 1
ID AAV90914 standard; protein; 269 AA.
XX
AC AAV90914;
XX
DT 30-AUG-2000 (first entry)
XX
DE Cenarchaeum symbiosum open reading frame protein sequence SEQ ID NO:6.
XX
KW Cenarchaeum symbiosum; non-thermophilic; crenarchaeote; physiology;
KW characterisation; archae; therapeutic; industrial; laboratory.
XX
OS Cenarchaeum symbiosum.
XX
PN WO200018909-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022752.
XX
PR 29-SEP-1998; 98US-0102294P.
XX
PA (DIVE-) DIVERSA CORP.
XX
PI Swanson RV, Feldman RA, Schleper C;
XX
DR WPI; 2000-293148/25.
XX
DR N-P-SDB; AA55189.
XX
PT New nucleic acids and proteins isolated from the non-thermophilic
PT crenarchaeote Cenarchaeum symbiosum, useful in characterizing the
PT physiology of these archae and in therapeutic, industrial or laboratory
PT techniques.
XX
PS Claim 24; Page 111-112; 210pp; English.
XX
CC AA55186 to AA55226 and AAV90913 to AAV90951 represent nucleic acids and
CC proteins isolated from the non-thermophilic crenarchaeote Cenarchaeum
CC symbiosum. The nucleic acids and proteins identified in the present
CC invention are useful in characterizing the physiology of these archae and
CC can be used in therapeutic, industrial or laboratory techniques. AA55227
CC to AA55260 represent promoter sequences from Cenarchaeum symbiosum.
CC AA55261 to AA55269 represent PCR primers and probes used in examples
CC from the present invention
XX
XX Sequence 269 AA;